*	PALM	INTR	ANET

Day : Monday Date: 7/24/2006

Time: 07:53:29

Inventor Information for 10/705476

Inventor Name	City	State/Country
ACHEN, MARC G.	FITZROY	AUSTRALIA
WILKS, ANDREW F.	SOUTH YARRA	AUSTRALIA
STACKER, STEVEN A.	NORTH FITZROY	AUSTRALIA
ALITALO, KARI	ESPOO	FINLAND

Applu line Contents Petition line Atty/Agent line Continuity/Reexem ? Foreign Continuity/Reexem ?
Search Another: Application# Search or Patent# Search
PCT / Search or PG PUBS # Search
Attorney Docket # Search.
Bar Code # Search

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SCORE Search Results Details for Application 10705476 and Search Result us-10-705-476-5.rag.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

July 5, 2006, 22:12:50; Search time 194 Seconds (without alignments)

834.302 Million cell updates/sec

Title:

US-10-705-476-5

Perfect score: 1963

Sequence:

1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:

2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:* 8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ક				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
			2			Aaw44293 Human vas
1	1963	100.0	354	2	AAW44293	Aaw49233 Human zve
2	1963	100.0	354	2	AAW49036	
3	1963	100.0	354	2	AAW53241	Aaw53241 Homo sapi
4	1963	100.0	354	3	AAB10649	Aab10649 Human VEG
5	1963	100.0	354	3	AAY70750	Aay70750 Human pre
6	1963	100.0	354	3	AAY70983	Aay70983 Human vas
7	1963	100.0	354	3	AAB29049	Aab29049 Human VEG
8	1963	100.0	354	4	AAB37606	Aab37606 Human VEG
9	1963	100.0	354	4	AAY97573	Aay97573 Human VEG
10	1963	100.0	354	4	AAU08441	Aau08441 Polypepti
11	1963	100.0	354	5	ABG33 05 5	Abg33055 Human vas
12	1963	100.0	354	5	ABG32046	Abg32046 Human Flt
13	1963	100.0	354	6	ABB84623	Abb84623 Human VEG
14	1963	100.0	354	7	ADD08 95 0	Add08950 Human VEG
15	1963	100.0	354	7	ADN95941	Adn95941 Human VEG
16	1963	100.0	354	8	ADQ20886	Adq20886 Human sof
17	1963	100.0	354	8	AD071602	Ado71602 A human v
18	1963	100.0	354	8	ADR31436	Adr31436 Human vas
19	1963	100.0	354	9	ADW80993	Adw80993 Human vas
20	1963	100.0	354	9	ADX69284	Adx69284 Human VEG
21	1963	100.0	354	9	ADZ00442	Adz00442 VEGF-D. 6
22	1963	100.0	354	9	ADZ79971	Adz79971 Human vas
23	1963	100.0	354	9	AEC08002	Aec08002 Human VEG
24	1963	100.0	354	9	AEC78160	Aec78160 Human VEG
25	1963	100.0	354	9	AED26685	Aed26685 Human VEG
26	1963	100.0	354	9	AED34383	Aed34383 Human vas
27	1963	100.0	354	9	AED12196	Aed12196 Vascular
28	1963	100.0	354	9	AED12194	Aed12194 Vascular
29	1963	100.0	354	10	AEF51599	Aef51599 VEGF-D, S
30	1926	98.1	354	4	AAB70685	Aab70685 Human vas
31	1917	97.7	620	2	AAW14994	Aaw14994 Human c-F
32	1804	91.9	325	2	AAW53240	Aaw53240 Homo sapi
33	1804	91.9	325	4	AAY97572	Aay97572 Human VEG
34	1675	85.3	358	2	AAW44295	Aaw44295 Mouse vas
35	1675	85.3	358	2	AAW53242	Aaw53242 Mus muscu
36	1675	85.3	358	5	AAM47930	Aam47930 Mouse VEG
37	1675	85.3	358	10	AEF51601	Aef51601 VEGF-D1 1
38	1671	85.1	358	2	AAW14992	Aaw14992 Murine c-
3 9	1608.5	81.9		2	AAY08286	Aay08286 Human gro
40	1525	77.7			ABG73779	Abg73779 Human NVR
41	1522	77.5	321		AAW53243	Aaw53243 Mus muscu
42	1522	77.5			AAM47931	Aam47931 Mouse VEG
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RESULT 1
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XX
AC
    AAW44293;
XX
     22-JUN-1998 (first entry)
DT
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OM protein - protein search, using sw model

Run on:

July 5, 2006, 22:21:40; Search time 49 Seconds (without alignments)

632.364 Million cell updates/sec

Title:

US-10-705-476-5

Perfect score: 1963

Sequence:

1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

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650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA: *

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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1963	100.0	354	2	US-08-915-795-5	Sequence 5, Appli

				_		_	
2	1963	100.0	354	2	US-09-296-275-5	Sequence	
3	1963	100.0	354	2	US-09-375-248-6	Sequence	
4	1963	100.0	354	2	US-09-468-647A-109	Sequence	
5	1963	100.0	354	2	US-09-169-079-22	Sequence	
6	1963	100.0	354	2	US-09-214-982-1	Sequence	
7	1963	100.0	354	2	US-09-427-657-4	Sequence	
8	1963	100.0	354	2	US-09-795-006A-119	Sequence	
9	1963	100.0	354	3	US-09-765-534B-22	Sequence	
10	1963	100.0	362	2	US-09-949-016-11286	Sequence	11286, A
11	1804	91.9	325	2	US-08-915-795-3	Sequence	3, Appli
12	1804	91.9	325	2	US-09-296-275-3	Sequence	3, Appli
13	1675	85.3	358	2	US-08-915-795-8	Sequence	
14	1675	85.3	358	2	US-09-847-524-2	Sequence	2, Appli
15	1675	85.3	358	2	US-09-296-275-8	Sequence	8, Appli
16	1675	85.3	358	2	US-09-438-046-15	Sequence	15, Appl
17	1522	77.5	321	2	US-08-915-795-9	Sequence	9, Appli
18	1522	77.5	321	2	US-09-847-524-4	Sequence	4, Appli
19	1522	77.5	321	2	US-09-296-275-9	Sequence	9, Appli
20	1087	55.4	197	2	US-09-431-888-8	Sequence	8, Appli
21	704.5	35.9	419	1	US-08-999-811-2	Sequence	2, Appli
22	704.5	35.9	419	2	US-09-042-105-2	Sequence	2, Appli
23	704.5	35.9	419	2	US-09-042-105-18	Sequence	18, Appl
24	704.5	35.9	419	2	US-08-795-430-8	Sequence	8, Appli
25	704.5	35.9	419	2	US-08-510-133A-35	Sequence	35, Appl
26	704.5	35.9	419	2	US-09-355-700-8	Sequence	8, Appli
27	704.5	35.9	419	2	US-08-601-132-33	Sequence	33, Appl
28	704.5	35.9	419	2	US-08-465-968-2	Sequence	2, Appli
29	704.5	35.9	419	2	US-08-671-573B-33	Sequence	33, Appl
30	704.5	35.9	419	2	US-09-438-046-14	Sequence	
31	704.5	35.9	419	2	US-09-631-092B-33	Sequence	33, Appl
32	704.5	35.9	419	2	US-10-084-488-2	Sequence	
33	704.5	35.9	419	2	US-10-084-488-18	Sequence	
34	704.5	35.9	419	2	US-09-375-248-4	Sequence	
35	704.5	35.9	419	2	US-09-468-647A-108	Sequence	
36	704.5	35.9	419	2	US-09-534-376A-8	Sequence	7.7
37	704.5	35.9	419	2	US-09-169-079-21	Sequence	
38	701.5	35.9	419	2	US-09-427-657-2	Sequence	
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42	704.5	35.9	419	2	US-09-219-442-2	Sequence	
43	704.5	35.9	419	3	US-09-765-534B-21	Sequence	
44	704.5	35.9	419	5	PCT-US96-09001-2	Sequence	
45	699.5	35.6	419	2	US-09-214-982-29	Sequence	
73	0,5.5	٠. د د	オエフ	4	00 00 211 002 20	Sequence	,

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RESULT 1
US-08-915-795-5
; Sequence 5, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
   APPLICANT: Marc G. ACHEN
    APPLICANT: Andrew F. WILKS
    APPLICANT: Steven A. STACKER
    APPLICANT: Kari ALITALO
    TITLE OF INVENTION: GROWTH FACTOR
    NUMBER OF SEQUENCES: 11
    CORRESPONDENCE ADDRESS:
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SCORE Search Results Details for Application 10705476 and Search Result us-10-705-476-5.rapbm.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

July 5, 2006, 22:33:36; Search time 185 Seconds (without alignments)

886 368 Million cell updates/sec

Title:

US-10-705-476-5

Perfect score: 1963

Sequence:

1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

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Total number of hits satisfying chosen parameters:

2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA_Main: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

왐 Query

Score Match Length DB ID

Description

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1 1963 100.0 354 3 US-09-956-095-2 Sequence 2, Appli 2 1963 100.0 354 3 US-09-219-345A-11 Sequence 11, Appl 3 1963 100.0 354 3 US-09-755-066A-119 Sequence 119, Appl 4 1963 100.0 354 3 US-09-755-248-6 Sequence 6, Appli 5 1963 100.0 354 3 US-09-755-534B-22 Sequence 22, Appl 6 1963 100.0 354 4 US-10-262-538-26 Sequence 26, Appl 7 1963 100.0 354 4 US-10-262-538-26 Sequence 27, Appl 8 1963 100.0 354 4 US-10-261-694-5 Sequence 5, Appli 9 1963 100.0 354 4 US-10-611-694-5 Sequence 5, Appli 10 1963 100.0 354 4 US-10-611-694-5 Sequence 5, Appli 11 1963 100.0 354 4 US-10-611-740-65 Sequence 5, Appli 11 1963 100.0 354 4 US-10-705-476-5 Sequence 5, Appli 12 1963 100.0 354 4 US-10-669-176-26 Sequence 22, Appli 13 1963 100.0 354 5 US-10-772-927A-18 Sequence 22, Appli 14 1963 100.0 354 5 US-10-772-927A-18 Sequence 27, Appli 15 1963 100.0 354 5 US-10-772-927A-18 Sequence 18, Appli 16 1963 100.0 354 5 US-10-783-860-3706 Sequence 3766, Appli 17 1963 100.0 354 5 US-10-868-577A-4 Sequence 4, Appli 17 1963 100.0 354 5 US-10-868-549-4 Sequence 4, Appli 18 1963 100.0 354 5 US-10-978-107-1 Sequence 10, Appli 1963 100.0 354 5 US-10-627-631-2 Sequence 2, Appli 1963 100.0 354 5 US-10-627-631-2 Sequence 7, Appl 22 1963 100.0 354 5 US-10-627-631-2 Sequence 7, Appl 23 1963 100.0 354 5 US-10-647-641 Sequence 60, Appl 24 1963 100.0 354 6 US-11-090-439-60 Sequence 70, Appl 25 1963 100.0 354 6 US-11-090-439-60 Sequence 70, Appl 26 1963 100.0 354 6 US-11-090-439-60 Sequence 60, Appl 27 1963 100.0 354 6 US-11-075-400-10 Sequence 119, Appl 1963 100.0 354 6 US-11-076-478-4 Sequence 4, Appli 1963 100.0 354 6 US-11-076-478-4 Sequence 4, Appli 1963 100.0 354 6 US-11-076-478-4 Sequence 4, Appli 1963 100.0 354 6 US-11-076-478-7 Sequence 8, Appli 1963 100.0 354 6 US-11-079-479-3 Sequence 8, Appli 1963 100.0 354 6 US-11-079-479-3 Sequence 8, Appli 1963 100.0 354 6 US-11-079-479-3 Sequence 8, Appli 1963
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RESULT 1
US-09-956-095-2
; Sequence 2, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
  APPLICANT: ACHEN, Marc G.
  APPLICANT: STACKER, Steven A.
  TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
  TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
  TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
  TITLE OF INVENTION: VASCULARIZATION OF TISSUE
```

SCORE Search Results Details for Application 10705476 and Search Result us-10-705-476-5.rapbn.

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<u>start</u>

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

July 5, 2006, 22:33:55; Search time 21 Seconds (without alignments)

452.312 Million cell updates/sec

Title:

US-10-705-476-5

Perfect score:

1963

Sequence:

1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

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Total number of hits satisfying chosen parameters:

112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	1963	100.0	354	6	US-10-505-928-866	Sequence 866, App
2	704.5	35.9	419	6	US-10-505-928-436	Sequence 436, App
3	704.5	35.9	419	6	US-10-505-928-864	Sequence 864, App
4	695.5	35.4	419	7	US-11-346-806-3	Sequence 3, Appli
5	169.5	8.6	147	7	US-11-346-806-4	Sequence 4, Appli
6	160.5	8.2	149	7	US-11-346-806-5	Sequence 5, Appli
7	160.5	8.2	170	6	US-10-505-928-584	Sequence 584, App
8	147	7.5	345	7	US-11-289-102-249	Sequence 249, App
9	115.5	5.9	426	6	US-10-449-902-54143	Sequence 54143, A
10	114.5	5.8	1093	6	US-10-449-902-41338	Sequence 41338, A
11	114.5	5.8	1287	6	US-10-505-928-341	Sequence 341, App
12	113	5.8	756	6	US-10-449-902-44363	Sequence 44363, A
13	112.5	5.7	259	7	US-11-217-997-34	Sequence 34, Appl
14	112.5	5.7	575	7	US-11-217-997-32	Sequence 32, Appl
15	112.5	5.7	1398	7	US-11-217-997-4	Sequence 4, Appli
16	112.5	5.7	1403	7	US-11-217-997-12	Sequence 12, Appl
17	112.5	5.7	1404	7	US-11-217-997-2	Sequence 2, Appli
18	112.5	5.7	1547	7	US-11-217-997-22	Sequence 22, Appl
19	112.5	5.7	1577	7	US-11-217-997-16	Sequence 16, Appl
20	112.5	5.7	1577	7	US-11-217-997-20	Sequence 20, Appl
21	112.5	5.7	1594	7	US-11-217-997-18	Sequence 18, Appl
22	112.5	5.7	1620	7	US-11-217-997-42	Sequence 42, Appl
23	112.5	5.7	1653	7	US-11-217-997-40	Sequence 40, Appl
24	111	5.7	2003	7	US-11-264-243-8	Sequence 8, Appli
25	108.5	5.5	342	7	US-11-038-753-1	Sequence 1, Appli
26	108	5.5	685	7 7	US-11-293-697-3546	Sequence 3546, Ap
27 28	105.5	5.4	1418 909	6	US-11-217-997-38	Sequence 38, Appl Sequence 44686, A
28 29	104.5 103.5	5.3 5.3	469	7	US-10-449-902-44686 US-11-246-999-41	Sequence 41, Appl
30	103.5	5.3	494	7	US-11-246-999-30	Sequence 30, Appl
31	103.5	5.3	567	7	US-11-246-999-50	Sequence 50, Appl
32	103.3	5.2	2556	7	US-11-264-243-6	Sequence 6, Appli
33	101.5	5.2	1218	7	US-11-178-724-21	Sequence 21, Appl
34	101.5	5.2	1218	7	US-11-071-796A-20	Sequence 20, Appl
	101.5	5.1	472	7	US-11-217-997-26	Sequence 26, Appl
36	101	5.1	2556	7	US-11-071-796A-22	Sequence 22, Appl
37	100.5	5.1	364	6	US-10-449-902-36200	Sequence 36200, A
38	100.5	5.1	1198	7	US-11-217-997-14	Sequence 14, Appl
39	100.5					Sequence 6, Appli
40	100	5.1	563	6	US-10-449-902-47820	Sequence 47820, A
41	100	5.1	563	6	US-10-449-902-55504	Sequence 55504, A
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43	98	5.0	314	6	US-10-953-349-10973	Sequence 10973, A
44	98	5.0	419	6	US-10-953-349-10972	Sequence 10972, A
45	98	5.0	422	6	US-10-953-349-10971	Sequence 10971, A

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; Sequence 866, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
  CURRENT APPLICATION NUMBER: US/10/505,928
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SCORE Search Results Details for Application 10705476 and Search Result us-10-705-476-5.ra

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This page gives you Search Results detail for the Application 10705476 and Search Result us-10-70 5.rapm.

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```
GenCore version 5.1.9
                 Copyright (c) 1993 - 2006 Biocceleration Ltd.
OM protein - protein search, using sw model
               July 5, 2006, 22:22:25; Search time 604 Seconds
Run on:
                                           (without alignments)
                                           894.938 Million cell updates/sec
Title:
               US-10-705-476-5
Perfect score: 1963
               1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354
Sequence:
Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
               8366291 seqs, 1526956180 residues
Searched:
                                                       8366291
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries
Database :
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                1: /EMC Celerra SIDS3/ptodata/2/paa/PCTUS COMB.pep:*
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                3: /EMC_Celerra_SIDS3/ptodata/2/paa/US073_COMB.pep:*
                4: /EMC Celerra SIDS3/ptodata/2/paa/US074 COMB.pep:*
               5: /EMC Celerra SIDS3/ptodata/2/paa/US075_COMB.pep:*
               6: /EMC_Celerra_SIDS3/ptodata/2/paa/US076_COMB.pep:*
                   /EMC_Celerra_SIDS3/ptodata/2/paa/US077_COMB.pep:*
                   /EMC Celerra SIDS3/ptodata/2/paa/US078 COMB.pep:*
                    /EMC_Celerra_SIDS3/ptodata/2/paa/US079_COMB.pep: *
                10: /EMC Celerra_SIDS3/ptodata/2/paa/US080_COMB.pep:*
                11: /EMC_Celerra_SIDS3/ptodata/2/paa/US081_COMB.pep:*
               12: /EMC_Celerra_SIDS3/ptodata/2/paa/US082_COMB.pep:*
               13: /EMC Celerra SIDS3/ptodata/2/paa/US083 COMB.pep:*
               14: /EMC_Celerra_SIDS3/ptodata/2/paa/US084_COMB.pep:*
                15: /EMC_Celerra_SIDS3/ptodata/2/paa/US085_COMB.pep:*
               16: /EMC Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*
               17: /EMC_Celerra_SIDS3/ptodata/2/paa/US087_COMB.pep:*
               18: /EMC_Celerra_SIDS3/ptodata/2/paa/US088_COMB.pep:*
               19: /EMC Celerra SIDS3/ptodata/2/paa/US089 COMB.pep:*
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```
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24:
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     /EMC Celerra SIDS3/ptodata/2/paa/US107 COMB.pep:*
     /EMC Celerra SIDS3/ptodata/2/paa/US108_COMB.pep:*
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51:
     /EMC_Celerra_SIDS3/ptodata/2/paa/US606_COMB.pep:*
     /EMC_Celerra_SIDS3/ptodata/2/paa/US607_COMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

		*				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
				- -		
1	1963	100.0	354	1	PCT-US00-14925-22	Sequence 22, Appl
2	1963	100.0	354	1	PCT-US03-36644-12	Sequence 12, Appl
3	1963	100.0	354	1	PCT-US03-38193-3706	Sequence 3706, Ap
4	1963	100.0	354	1	PCT-US05-10109-60	Sequence 60, Appl
5	1963	100.0	354	1	PCT-US05-10109-62	Sequence 62, Appl
6	1963	100.0	354	1	PCT-US05-47288-49	Sequence 49, Appl
7	1963	100.0	354	1	PCT-US97-14696-5	Sequence 5, Appli
8	1963	100.0	354	1	PCT-US99-06133-6	Sequence 6, Appli
9	1963	100.0	354	17	US-08-759-657-2	Sequence 2, Appli
10	1963	100.0	354	19	US-08-933-455-2	Sequence 2, Appli
11	1963	100.0	354	22	US-09-219-345A-11	Sequence 11, Appl
12	1963	100.0	354	22	US-09-219-345B-10	Sequence 10, Appl
13	1963	100.0	354	27	US-09-791-537-91625	Sequence 91625, A
14	1963	100.0	354	29	US-09-956-095-2	Sequence 2, Appli
15	1963	100.0	354	31	US-10-161-694-5	Sequence 5, Appli
16	1963	100.0	354	32	US-10-262-538-26	Sequence 26, Appl
17	1963	100.0	354	32	US-10-262-538A-26	Sequence 26, Appl
18	1963	100.0	354	32	US-10-274-953-5	Sequence 5, Appli

SCORE Search Results Details for Application 10705476 and Search Result us-10-705-476-5.rapn.

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This page gives you Search Results detail for the Application 10705476 and Search Result us-10-705-476-5.rapn.

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```
GenCore version 5.1.9
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```

OM protein - protein search, using sw model

Run on:

July 5, 2006, 22:23:20; Search time 24 Seconds (without alignments)

592.798 Million cell updates/sec

Title:

US-10-705-476-5

Perfect score: 1963

Sequence:

1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

179241 seqs, 40189672 residues

Total number of hits satisfying chosen parameters:

179241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Result

Pending_Patents_AA_New: *

1: /EMC_Celerra_SIDS3/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /EMC Celerra_SIDS3/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/paa/US10_NEW_COMB.pep:*

/EMC Celerra_SIDS3/ptodata/1/paa/US11_NEW_COMB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ouerv

No.	Score	Match	Length	DB	ID	Description
	1063	100 0	254	8	US-60-808-106-52	Sequence 52, Appl
1 2	1963 704.5	100.0 35.9	354 419	5	US-09-499-468-2	Sequence 2, Appli
3	704.5	35.9	419	7	US-11-429-373-570	Sequence 570, App
4	704.5	35.9	419	7	US-11-429-373-571	Sequence 571, App
5	704.5	35.9	419	7	US-11-429-373-573	Sequence 573, App
6	704.5	35.9	419	7	US-11-429-373-574	Sequence 574, App
7	704.5	35.9	419	7	US-11-429-374-570	Sequence 570, App
8	704.5	35.9	419	7	US-11-429-374-571	Sequence 571, App
9	704.5	35.9	419	7	US-11-429-374-573	Sequence 573, App
10	704.5	35.9	419	7	US-11-429-374-574	Sequence 574, App
11	704.5	35.9	419	7	US-11-429-276-570	Sequence 570, App
12	704.5	35.9	419	7	US-11-429-276-571	Sequence 571, App
13	704.5	35.9	419	7	US-11-429-276-573	Sequence 573, App
14	704.5	35.9	419	7	US-11-429-276-574	Sequence 574, App
15	704.5	35.9	419	8	US-60-808-106-51	Sequence 51, Appl
16	664.5	33.9	350	5	US-09-499-468-4	Sequence 4, Appli
17	421.5	21.5	734	7	US-11-429-373-354	Sequence 354, App
18	421.5	21.5	734	7	US-11-429-373-357	Sequence 357, App
19	421.5	21.5	734	7	US-11-429-374-354	Sequence 354, App
20	421.5	21.5	734	7	US-11-429-374-357	Sequence 357, App
21	421.5	21.5	734	7	US-11-429-276-354	Sequence 354, App
22	421.5	21.5	734	7	US-11-429-276-357	Sequence 357, App
23	413	21.0	734	7	US-11-429-373-355	Sequence 355, App
24	413	21.0	734	7	US-11-429-373-358	Sequence 358, App
25	413	21.0	734	7	US-11-429-374-355	Sequence 355, App
26	413	21.0	734	7	US-11-429-374-358	Sequence 358, App
27	413	21.0	73.4 73.4	7 7	US-11-429-276-355	Sequence 355, App
28 29	413 204	21.0 10.4	165	7	US-11-429-276-358	Sequence 358, App Sequence 8, Appli
30	204 204	10.4	165	8	US-11-414-782-8 US-60-808-106-4	Sequence 4, Appli
31	204	10.4	165	8	US-60-808-106-22	Sequence 22, Appl
32	204	10.4	191	6	US-10-207-655A-51	Sequence 51, Appl
33	204	10.4	191	7	US-11-441-790-1	Sequence 1, Appli
34	204	10.4	191	7	US-11-207-655-51	Sequence 51, Appl
35	204	10.4	191	8	US-60-808-106-2	Sequence 2, Appli
36	204	10.4	191	8	US-60-808-106-21	Sequence 21, Appl
37	203	10.3	190	8	US-60-808-106-33	Sequence 33, Appl
38	201	10.2	183	7	US-11-414-782-7	Sequence 7, Appli
39	201	10.2	183	8	US-60-808-106-15	Sequence 15, Appl
40	201	10.2	209	8	US-60-808-106-14	Sequence 14, Appl
41	200.5	10.2	206	7	US-11-414-782-5	Sequence 5, Appli
42	200.5	10.2	206	8	US-60-808-106-19	Sequence 19, Appl
43	200.5	10.2	232	5	US-09-499-468-7	Sequence 7, Appli
44	200.5	10.2	232	8	US-60-808-106-18	Sequence 18, Appl
45	200	10.2	164	8	US-60-808-106-25	Sequence 25, Appl

```
RESULT 1
US-60-808-106-52
; Sequence 52, Application US/60808106
; GENERAL INFORMATION:
; APPLICANT: Szkudlinski, Mariusz W.
; APPLICANT: Weintraub, Bruce
; TITLE OF INVENTION: VEGF Analogs and Methods of Use
; FILE REFERENCE: TROP-005/01US
; CURRENT APPLICATION NUMBER: US/60/808,106
```

SCORE Search Results Deta

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This page gives you Search Results detail for the Application 10705476 and Search Result us-10-70 start

> GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

July 5, 2006, 22:16:40; Search time 41 Seconds

(without alignments)

830.750 Million cell updates/sec

US-10-705-476-5 Title:

Perfect score: 1963

Sequence: 1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80:*

1: pir1:* 2: pir2:* 3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		₹				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
						1
1	704.5	35.9	419	2	S69207	vascular endotheli
2	200.5	10.2	232	2	A41551	vascular endotheli
3	200	10.2	190	2	B40080	vascular endotheli
4	198	10.1	190	2	S52130	vascular endotheli
5	198	10.1	190	2	B44881	vascular endotheli
6	198	10.1	214	2	A44881	vascular endotheli
7	194	9.9	190	2	A35987	glioma-derived vas
8	181.5	9.2	1700	2	S08167	Balbiani ring 3 pr

9	176.5	9.0	188	2	JC4680	vascular endotheli
10	167.5	8.5	146	2	S57956	ovine vascular end
11	166.5	8.5	120	2	A33787	vascular endotheli
12	164	8.4	148	2	D49530	16K vascular endot
13	161	8.2	245	1	TVCTSS	platelet-derived q
14	160.5	8.2	149	2	A41236	placental growth f
15	158	8.0	158	2	A56125	placental growth f
16	147.5	7.5	207	2	JC4679	vascular endotheli
17	145	. 7.4	133	2	B49530	vascular endotheli
18	145	7.4	241	1	PFHUG2	platelet-derived g
19	139.5	7.1	1187	2	T18355	hypothetical prote
20	135.5	6.9	241	1	PFMSGB	platelet-derived g
21	133.5	6.8	225	2	S25097	platelet-derived g
22	130.5	6.6	370	2	JC7592	spinal cord-derive
23	128	6.5	748	2	S66129	disintegrin (EC 3.
24	125.5	6.4	196	2	B28964	platelet-derived g
25	125.5	6.4	211	1	PFHUG1	platelet-derived g
26	125.5	6.4	2946	2	T15840	hypothetical prote
27	123.5	6.3	370	2	JC7591	spinal cord-derive
28	123.3	6.2	226	1	TVMVSS	PDGF-related trans
29	120.5	6.1	160	2	JQ0542	185K secretory pro
30	120.5	6.1	200	2	I51551	platelet-derived q
31	120	6.1	215	2	S08220	platelet derived g
32	120	6.1	215	2	I51550	platelet-derived g
33	119.5	6.1	1106	2	T44598	hypothetical prote
34	119.5	6.0	965	2	S62935	hypothetical prote
35	117.5	6.0	370	2	JC7998	platelet-derived g
36	117.5	5.9	1548	2	S34583	serine proteinase
37	115.5	5.9	1964	2	T09059	notch4 - mouse
38	114.5	5.8	1287	2	A41685	SIL protein - huma
39	114.5	5.8	5376	2	T42215	zonadhesin - mouse
40	114.5	5.8	197	2	S25096	platelet-derived g
41	113	5.8	846	2	A30889	integrin beta chai
42	112.5	5.7	2195	2	T34264	hypothetical prote
42	112.5	5.7 5.7	3635	2	T10053	laminin alpha 5 ch
43	111.5	5.7 5.7	336	2	D69074	polyferredoxin 4x2
				2	T27684	
45	111.5	5.7	2219	2	12/684	hypothetical prote

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RESULT 1
S69207
vascular endothelial growth factor C precursor - human
N; Alternate names: FLT4 ligand DHM
C; Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C; Accession: S69207; S61795; S71443; S69208; G02659
R; Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela
EMBO J. 15, 1751, 1996
A; Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand
A; Reference number: S69207; MUID: 96203094; PMID: 8612600
A; Accession: S69207
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A;Residues: 1-419
A;Cross-references: UNIPROT:P49767; UNIPARC:UPI0000001C2A; EMBL:X94216; NID:g1177488;
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A; Note: only a part of the translation is shown
A; Note: this is a revision to the sequence from reference S61795
```